

REMARKS

Claims 20-30 and 32-39 are pending in the application. Claims 22-28 and 32-39 are withdrawn as being drawn to non-elected inventions. Claims 20, 21, 29 and 30 are under active consideration. Claim 31 has been canceled and claim 20 has been amended as suggested by the Examiner to recite "endooligopeptidase A activity" to further clarify the intended subject matter of the claimed invention. This amendment addresses the rejections under 35 U.S.C. § 112, first and second paragraphs. Support for the amendment to claim 20 can be found in the specification, for example, at page 16, lines 14-19, and in Figure 5 which points out regions of homology between SEQ ID NO:1 and *Oryctolagus cuniculus* endooligopeptidase A (g2827886), and at page 51, line 26 through page 52, line 10, which describes assays for measuring protease activity. In addition, a recent Blast analysis (Exhibit A) shows that SEQ ID NO:1 is 100% identical from residues 1 to 345 to human endooligopeptidase A (g28932237). The Examiner has indicated that this amendment would put all of the elected claims in condition for allowance (Final Office Action at page 3).

The present amendment does not introduce new issues, and places the subject application in condition for allowance and/or simplifies issues for appeal. Accordingly, entry of the amendment is proper and respectfully requested. Applicants reserve the right to prosecute non-elected subject matter in subsequent divisional applications.

Rejoinder of Claims

The Examiner is reminded that claims 32, 35, 38, and 39, drawn to methods of using the polypeptides of Group I should be rejoined per the Commissioner's Notice in the Official Gazette of March 26, 1996, entitled "Guidance on Treatment of Product and Process Claims in light of *In re Ochiai*, *In re Brouwer* and 35 U.S.C. § 103(b)" which sets forth the rules, upon allowance of any product claim, for rejoinder of process claims covering the same scope of products. Applicants request that claims 32, 35, 38, and 39 be rejoined and examined upon allowance of any claim drawn to the polypeptides of Group I.

Rejection under 35 U.S.C. § 112, second paragraph

Claims 20, 21, 29, and 30 have been rejected under 35 U.S.C. § 112, second paragraph, as allegedly being indefinite in the recitation of the term "endooligopeptidase activity" on the

grounds that “[t]here are two potential meanings of this term within the context of the instant invention” (Final Office Action, page 2). The Examiner has stated that if the claim were amended to recite endooligopeptidase A activity, “[a]mendment as such would put all of the elected claims in condition for allowance” (Final Office Action, page 3). In order to expedite prosecution, claim 20 has been amended as suggested by the Examiner to recite “endooligopeptidase A activity.” Therefore, withdrawal of the rejection under U.S.C. § 112, second paragraph is respectfully requested.

Written description and Enablement Rejections under 35 U.S.C. § 112, first paragraph

Claims 20 and 29 have been rejected under the first paragraph of 35 U.S.C. 112 for alleged lack of adequate written description and enablement. These rejections are respectfully traversed for the reasons previously made of record in the response to the Office Action of March 27, 2003 and on the following grounds.

In order to expedite prosecution, claim 20 has been amended as suggested by the Examiner to recite “endooligopeptidase A activity.” The Examiner has stated that this amendment would put the elected claims in condition for allowance because “one would consider the disclosed species of SEQ ID NO:1 to be representative of a genus of variants having high similarity in both structure and function and one would know how to use all such variants” (Final Office Action, page 4). Therefore, withdrawal of the rejections under U.S.C. § 112, first paragraph is respectfully requested.

CONCLUSION

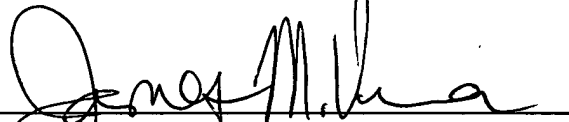
In light of the above amendments and remarks, Applicants submit that the present application is fully in condition for allowance, and request that the Examiner withdraw the outstanding objections/rejections. Early notice to that effect is earnestly solicited.

If the Examiner contemplates other action, or if a telephone conference would expedite allowance of the claims, Applicants invite the Examiner to contact the undersigned at the number listed below.

Applicants believe that no fee is due with this communication. However, if the USPTO determines that a fee is due, the Commissioner is hereby authorized to charge Deposit Account No. **09-0108**.

Respectfully submitted,

INCYTE CORPORATION

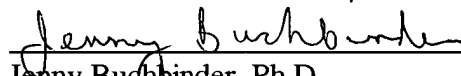


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Date: December 5, 2003



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Date: December 5, 2003

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EXHIBIT A

Docket No.: PF-0513-1 DIV
USN: 09/713,669**SeqServer**
biology in silico**BLAST2 Search Results**[Sequences](#)[Help](#)[Retrieval](#)[BLAST2](#)[FASTA](#)[ClustalW](#)[CGC Assembly](#)[Phrap](#)[Translation](#)[BLAST2 Manual](#)

Confidential -- Property of Incyte Corporation SeqServer Version 4.6 Jan 2002

Program: blastp**Sequence ID(s):**☐ 031381CD1 vs. genpept137

NCBI-BLASTP 2.0.10 [Aug-26-1999]



Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= 031381CD1
(459 letters)Database: genpept137
1,534,369 sequences; 474,463,515 total letters

Searching.....done

Sequences producing significant alignments:	Score (bits)	E Value
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<input checked="" type="checkbox"/> g21438866 unnamed protein product [Homo sapiens]	680	0.0
<input checked="" type="checkbox"/> g12043569 Nudel [Homo sapiens]	680	0.0
<input checked="" type="checkbox"/> g12002978 mitotin-associated protein MITAP1 [Homo sapiens]	680	0.0
<input checked="" type="checkbox"/> g19913485 NudE nuclear distribution gene E homolog like 1 (A.	677	0.0
<input checked="" type="checkbox"/> g13784950 endooligopeptidase A protein [Oryctolagus cuniculu	672	0.0
<input checked="" type="checkbox"/> g9965368 Nudel [Mus musculus]	655	0.0
<input checked="" type="checkbox"/> g28386182 Nudel protein [Mus musculus]	653	0.0
<input checked="" type="checkbox"/> g15822547 LIS1-interacting protein NUDE2 [Rattus norvegicus]	653	0.0
<input checked="" type="checkbox"/> g11992277 NUDE-like protein [Mus musculus]	653	0.0

>[g28932237](#) endooligopeptidase A [Homo sapiens]
Length = 345Score = 680 bits (1736), Expect = 0.0
Identities = 345/345 (100%), Positives = 345/345 (100%)

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Sbjct: 121 ANDDLERAKRATIVSLEDFEQRLNQAIERNAFLESELDEKESLLVSVQRLKDEARDLRQE 180

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Sbjct: 181 LAVRERQQEVTRKSAPSSPTLDCEKMSAVQASLSLPATPVGKGTENTFPSPKAI PNGFG 240

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Sbjct: 241 TSPLTPSARISALNIVGDLLRKVGALLESKLAACRNFAKDQASRKSYSIGNVNCGVNLNG 300

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TKFSRSGHTSFFDKGAVNGFDPAPPPPGLGSSRPSSAPGMLPLSV 345

Sbjct: 301 TKFSRSGHTSFFDKGAVNGFDPAPPPPGLGSSRPSSAPGMLPLSV 345

>g21438866 unnamed protein product [Homo sapiens]
Length = 345

Score = 680 bits (1736), Expect = 0.0
Identities = 345/345 (100%), Positives = 345/345 (100%)

Query: 1 MDGEDIPDFSSSLKEETAYWKELSLKYKQSFQEARDELVEFQEGSRELEAELEAQLVQAEQ 60
MDGEDIPDFSSSLKEETAYWKELSLKYKQSFQEARDELVEFQEGSRELEAELEAQLVQAEQ 60

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Sbjct: 61 RNRDLQADNQRLKYEVEALKEKLEHQAQSYKQVSVLEDDLSQTRAIKEQLHKYVRELEQ 120

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ANDDLERAKRATIVSLEDFEQRLNQAIERNAFLESELDEKESLLVSVQRLKDEARDLRQE 180

Sbjct: 121 ANDDLERAKRATIVSLEDFEQRLNQAIERNAFLESELDEKESLLVSVQRLKDEARDLRQE 180

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Sbjct: 181 LAVRERQQEVTRKSAPSSPTLDCEKMSAVQASLSLPATPVGKGTENTFPSPKAI PNGFG 240

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Sbjct: 301 TKFSRSGHTSFFDKGAVNGFDPAPPPPGLGSSRPSSAPGMLPLSV 345

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Sbjct: 1 MDGEDIPDFSSSLKEETAYWKELSLKYKQSFQEARDELVEFQEGSRELEAELEAQLVQAEQ 60

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Query: 181 LAVRERQQEVTRKSAPSSPTLDCEKMDSAVQASLSLPATPVGKGTENTFPSPKAIPNGFG 240
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Sbjct: 181 LAVRERQQEVTRKSAPSSPTLDCEKMDSAVQASLSLPATPVGKGTENTFPSPKAI PNGFG 240

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Sbjct: 241 TSPLTPSARISALNIVGDLLRKVGALSKLAACRNFAKDQASRKSYSIGNVNCVNLNGNG 300

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Sbjct: 61 RNRDLQADNQRLLKYEVEALKEKLEHQAQSYQVSVLEDDLSQTRAIKEQLHKYVRELEQ 120

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Query: 181 LAVRERQQEVTRKSAPSSPTLDCEKMDSAVQASLSLPATPVGKGTENTFPSPKAI PNGFG 240
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TSPLTPSARISALNIVGDLLRKVGALSKLAACRNFAKDQASRKSYSIGNVNCV+N NG

Sbjct: 241 TSPLTPSARISALNIVGDLLRKVGALSKLAACRNFAKDQASRKSYSIGNVNCVNMNSNG 300

Query: 301 TKFSRSGHTSFFDKGAVNGFDPAPPPPGLGSSRPSSAPGMLPLSV 345
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Sbjct: 301 TKFSRSGHTSFFDKGAVNGFDPAPPPPGLGSSRPLSAPGMLPLSV 345

>g9965368 Nudel [Mus musculus]
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Sbjct: 1 MDGEDIPDFSSLKEETAYWKELSLKYKQSFQEARDELVEFQEGSRELEAELEAQLVQAEQ 60

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Sbjct: 61 RNRDLQADNQRLLKYEVEALKEKLEHQAQSYQVSVLEDDLSQTRAIKEQLHKYVRELEQ 120

Query: 121 ANDDLERAKRATIVSLEDFEQRLNQAIERNAFLESELDEKESLLVSVQRLKDEARDLRQE 180

ANDDLERAKRATIVSLEDFEQRLNQAIERNAFLESELDEKESLLVSVQRLKDEARDLRQE
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Query: 241 TSPLTPSARISALNIVGDLLRKVGALSKLAACRNFAKDQASRKSYSIGNVNCVNLNGNG 300
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Query: 301 TKFSRSGHTSFFDKGAVNGFDPAPPPPGLGSSRPSSAPGMLPLSV 345
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Sbjct: 1 MDGEDIPDFSSSLKEETAYWKELSLKYKQSFQEARDELVEFQEGSRELEAELEAQLVQAEQ 60

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RNRDLQADNQRLKYEVEALKEKLEHQAQSYKQVSVLEDDLSQTRAIKEQLHKYVRELEQ
Sbjct: 61 RNRDLQADNQRLKYEVEALKEKLEHQAQSYKQVSVLEDDLSQTRAIKEQLHKYVRELEQ 120

Query: 121 ANDDLERAKRATIVSLEDFEQRLNQAIERNAFLESELDEKESLLVSVQRLKDEARDLRQE 180
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Sbjct: 121 ANDDLERAKRATIVSLEDFEQRLNQAIERNAFLESELDEKESLLVSVQRLKDEARDLRQE 180

Query: 181 LAVRERQQEVTRKSAPSSPTLDCEKMDSAVQASLSLPATPVGKGTENTFPSPKAI PNGFG 240
LAVRERQQEVTRKSAPSSPTLDCEKMDSAVQASLSLPATPVGKGTEN+FPSPKAI PNGFG
Sbjct: 181 LAVRERQQEVTRKSAPSSPTLDCEKMDSAVQASLSLPATPVGKGTENSFPSPKAI PNGFG 240

Query: 241 TSPLTPSARISALNIVGDLLRKVGALSKLAACRNFAKDQASRKSYSIGNVNCVNLNGNG 300
TSPLTPSARISALNIVGDLLRKVGALSKLAACRNFAKDQASRKSYSIGNVNCVNLNGNG
Sbjct: 241 TSPLTPSARISALNIVGDLLRKVGALSKLAACRNFAKDQASRKSYSVPGSVNCGVMNSNG 300

Query: 301 TKFSRSGHTSFFDKGAVNGFDPAPPPPGLGSSRPSSAPGMLPLSV 345
+ RSG +FF KGAVNGFDPAPPPPGLGSSRPSSAPGMLPLSV
Sbjct: 301 PECPRSGRATFFHKGAVNGFDPAPPPPGLGSSRPSSAPGMLPLSV 345

>g15822547 LIS1-interacting protein NUDE2 [Rattus norvegicus]
Length = 345

Score = 653 bits (1667), Expect = 0.0
Identities = 331/345 (95%), Positives = 337/345 (96%)

Query: 1 MDGEDIPDFSSSLKEETAYWKELSLKYKQSFQEARDELVEFQEGSRELEAELEAQLVQAEQ 60
MDGEDIPDFSSSLKEETAYWKELSLKYKQSFQEARDELVEFQEGSRELEAELEAQLVQAEQ
Sbjct: 1 MDGEDIPDFSSSLKEETAYWKELSLKYKQSFQEARDELVEFQEGSRELEAELEAQLVQAEQ 60

Query: 61 RNRDLQADNQRLKYEVEALKEKLEHQAQSYKQVSVLEDDLSQTRAIKEQLHKYVRELEQ 120
RNRDLQADNQRLKYEVEALKEKLEHQAQSYKQVSVLEDDLSQTRAIKEQLHKYVRELEQ
Sbjct: 61 RNRDLQADNQRLKYEVEALKEKLEHQAQSYKQVSVLEDDLSQTRAIKEQLHKYVRELEQ 120

Query: 121 ANDDLERAKRATIVSLEDFEQRLNQAIERNAFLESELDEKESLLVSVQRLKDEARDLRQE 180
ANDDLERAKRATIVSLEDFEQRLNQAIERNAFLESELDEKESLLVSVQRLKDEARDLRQE
Sbjct: 121 ANDDLERAKRATIVSLEDFEQRLNQAIERNAFLESELDEKESLLVSVQRLKDEARDLRQE 180

Query: 181 LAVRERQQEVTRKSAPSSPTLDCEKMSAVQASLSLPATPVGKGTENTFPSPKAI PNGFG 240
LAVRERQQEVTRKSAPSSPTLDCEKMSAVQASLSLPATPVGKGTEN+FPSPKAI PNGFG
Sbjct: 181 LAVRERQQEVTRKSAPSSPTLDCEKMSAVQASLSLPATPVGKGTENSFPSPKAI PNGFG 240

Query: 241 TSPLTPSARISALNIVGDLLRKVGAKESKLAACRNFAKDQASRKSYSIGNVNCGVNLNG 300
TSPLTPSARISALNIVGDLLRKVGAKESKLAACRNFAKDQASRKS+ G+VNCGV+N NG
Sbjct: 241 TSPLTPSARISALNIVGDLLRKVGAKESKLAACRNFAKDQASRKSYPGVSNCVNMNSNG 300

Query: 301 TKFSRSGHTSFFDKGAVNGFDPAPPPPGLGSSRPSSAPGMLPLSV 345
+ RSG +FF KGAVNGFDPAPPPPGLGSSRPSSAPGMLPLSV
Sbjct: 301 PECPRSGRATFFHKGAVNGFDPAPPPPGLGSSRPSSAPGMLPLSV 345

>g11992277 NUDE-like protein [Mus musculus]
Length = 345

Score = 653 bits (1667), Expect = 0.0

Identities = 331/345 (96%), Positives = 337/345 (98%)

Query: 1 MDGEDIPDFSSLKEETAYWKELSLKYKQSFQEARDELVEFQEGSRELEAELEAQLVQAEQ 60
MDGEDIPDFSSLKEETAYWKELSLKYKQSFQEARDELVEFQEGSRELEAELEAQLVQAEQ
Sbjct: 1 MDGEDIPDFSSLKEETAYWKELSLKYKQSFQEARDELVEFQEGSRELEAELEAQLVQAEQ 60

Query: 61 RNRDLQADNQLKYEVEALKEKLEHQAQSYKQVSVLEDDLSQTRAIKEQLHKYVRELEQ 120
RNRDLQADNQLKYEVEALKEKLEHQAQSYKQVSVLEDDLSQTRAIKEQLHKYVRELEQ
Sbjct: 61 RNRDLQADNQLKYEVEALKEKLEHQAQSYKQVSVLEDDLSQTRAIKEQLHKYVRELEQ 120

Query: 121 ANDDLERAKRATIVSLEDQEQRLNQAIRNAFLSELEDEKESLLVSVQRLKDEARDLRQE 180
ANDDLERAKRATIVSLEDQEQRLNQAIRNAFLSELEDEKESLLVSVQRLKDEARDLRQE
Sbjct: 121 ANDDLERAKRATIVSLEDQEQRLNQAIRNAFLSELEDEKESLLVSVQRLKDEARDLRQE 180

Query: 181 LAVRERQQEVTRKSAPSSPTLDCEKMSAVQASLSLPATPVGKGTENTFPSPKAI PNGFG 240
LAVRERQQEVTRKSAPSSPTLDCEKMSAVQASLSLPATPVGKGTEN+FPSPKAI PNGFG
Sbjct: 181 LAVRERQQEVTRKSAPSSPTLDCEKMSAVQASLSLPATPVGKGTENSFPSPKAI PNGFG 240

Query: 241 TSPLTPSARISALNIVGDLLRKVGAKESKLAACRNFAKDQASRKSYSIGNVNCGVNLNG 300
TSPLTPSARISALNIVGDLLRKVGAKESKLAACRNFAKDQASRKS+ G+VNCGV+N NG
Sbjct: 241 TSPLTPSARISALNIVGDLLRKVGAKESKLAACRNFAKDQASRKSYPGVSNCVNMNSNG 300

Query: 301 TKFSRSGHTSFFDKGAVNGFDPAPPPPGLGSSRPSSAPGMLPLSV 345
+ RSG +FF KGAVNGFDPAPPPPGLGSSRPSSAPGMLPLSV
Sbjct: 301 PECPRSGRATFFHKGAVNGFDPAPPPPGLGSSRPSSAPGMLPLSV 345

Database: genpept137

Posted date: Sep 11, 2003 11:22 AM

Number of letters in database: 474,463,515

Number of sequences in database: 1,534,369

Lambda	K	H
0.314	0.131	0.382

Gapped

Lambda	K	H
0.270	0.0470	0.230

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 447652329

Number of Sequences: 1534369

Number of extensions: 21204658

Number of successful extensions: 134228

Number of sequences better than 10.0: 6015

Number of HSP's better than 10.0 without gapping: 655

Number of HSP's successfully gapped in prelim test: 5532
Number of HSP's that attempted gapping in prelim test: 104327
Number of HSP's gapped (non-prelim): 23265
length of query: 459
length of database: 474,463,515
effective HSP length: 62
effective length of query: 397
effective length of database: 379,332,637
effective search space: 150595056889
effective search space used: 150595056889
T: 11
A: 40
X1: 16 (7.3 bits)
X2: 38 (14.8 bits)
X3: 64 (24.9 bits)
S1: 42 (22.0 bits)

Graphical Viewer

Submit sequences to:

